Human microbiome-derived peptide affects the development of experimental autoimmune encephalomyelitis via molecular mimicry

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Abstract

Background: Gut commensal microbiota has been identified as a potential environmental risk factor for multiple sclerosis (MS), and numerous studies have linked the commensal microorganism with the onset of MS. However, little is known about the mechanisms underlying the gut microbiome and host-immune system interaction. **Results:** Here, we introduce the concept of molecular mimicry to address this issue by mining human microbial-derived peptides based on their similarity to the MHC II-TCR binding pattern of self-antigens. We analyzed 304,246 human microbiome genomes and 103 metagenomes collected from the MS cohort and identified 731 nonredundant analogs of myelin oligodendrocyte glycoprotein peptide 35-55 (MOG_{35-55}). Of note, half of these analogs could bind to MHC II and interact with TCR through structural modeling of the interaction using fine-tuned AlphaFold. Among the 8 selected peptides, the peptide (P3) derived from human gut commensal *Akkermansia muciniphila* shows the ability to activate MOG_{35-55}-specific $CD4^+$ T cells *in vitro* and exacerbate the development of experimental autoimmune encephalomyelitis (EAE) in mice. Furthermore, dendritic cells could process and present P3 to MOG-specific $CD4^+$ T cells and activate these cells. Collectively, our data suggests the potential involvement of a MOG_{35-55}-mimic peptide derived from the gut microbiota as a molecular trigger of EAE pathogenesis. **Conclusions:** Our findings offer direct evidence of how microbes can initiate the development of EAE, suggesting a potential microbiome-based therapeutic target for inhibiting the

progression of MS.

Keywords: multiple sclerosis, experimental autoimmune encephalomyelitis, molecular mimicry, gut microbiota

Introduction

Multiple sclerosis (MS) is an autoimmune disease characterized by the involvement of autoreactive T cells targeting myelin antigens, leading to the destruction of myelin and damage to axons, resulting in neurologic syndromes and physical disability (1). The global prevalence of MS stands at approximately 2.8 million individuals (2), with an increasing incidence observed in developing countries and among children (3). Although the etiology of MS remains unknown, both genetic and environmental factors have been implicated in its development (1). Accumulating evidence suggests that gut microorganisms play a pathogenic role in MS (4, 5). Research has found notable differences in the composition of gut bacteria between MS patients and healthy individuals (6, 7). Similar alterations in the gut microbiota, including elevated levels of *Akkermansia muciniphila* (*A. muciniphila*), have also been observed in experimental autoimmune encephalomyelitis (EAE), an animal model employed to investigate MS (8). However, how the alterations in the gut microbiota might affect MS/EAE development remains largely unknown.

Molecular mimicry is one of the leading mechanisms in linking the role of microbiota

in immune reactivity in autoimmune diseases and cancer (9-13). Reassuringly, it has been reported that microbiota-derived peptides resembling myelin basic protein (MBP) can activate autoreactive T cells in MS (14-16). MBP, along with proteolipid protein (PLP) and myelin oligodendrocyte glycoprotein (MOG), are myelin antigens targeted by HLA-DR-restricted T cells, leading to MS development (1). Of note, MOG has been considered a primary target of cellular and humoral immune responses in multiple diseases due to its special extracellular immunoglobulin domain, which is directly accessible to binding partners including antibodies (17-19). Furthermore, MOG 35-55 (MOG_{35-55}) peptide has been widely used to induce EAE. Intrigued by these findings, we hypothesized that microbiome-derived peptides resembling the MOG_{35-55} epitope could trigger the autoimmune response responsible for initiating EAE.

To address this hypothesis, we analyzed human microbiome genomes and metagenome databases collected from MS cohort. Our aim was to identify microbial peptides with MHC II-TCR recognition patterns resembling those of MOG_{35-55}, which is presented by the MHC class II I-A^b and induces chronic EAE in C57BL/6J mice (20). Subsequently, we identified, synthesized, and tested 8 of these peptides for their ability to activate MOG_{35-55}-specific T cells. Our findings revealed that a predicted peptide (P3) derived from the gut commensal organism *A. muciniphila* can activate mouse MOG_{35-55}-specific T cells *in vitro*, albeit to a lesser extent compared to the MOG_{35-55} peptide. Additionally, P3 immunization can exacerbate the

development of EAE. We also observed some cross-reactivity between MOG_{35-55} peptide and $CD4^+$ T cells obtained from mice immunized with P3. Furthermore, dendritic cells (DCs) were able to process P3 and present it to $CD4^+$ T cells isolated from 2D2 mice expressing a MOG-specific T cell receptor. Our findings suggest that microbial peptide derived from the gut commensal, resembling MOG_{35-55}, may mimic the native myelin peptide and potentially contribute to the EAE development.

Results

Well-defined peptide-MHC II-TCR binding motifs guided microbiome-derived epitope discovery from the human microbiome

To uncover the microbiome-derived epitopes resembling the immunodominant MOG_{35-55} peptide, we designed a genome mining workflow involving an analysis of a vast dataset comprising 304,246 human microbiome genomes (21, 22) and 103 metagenomic samples from a MS study cohort (23) (Fig 1A). We first extracted 404,181 MOG_{35-55} analogs (Supplementary table 1) from these resources, followed by a filtering process that retained 21,557 analogs (3,946 non-redundant sequences) possessing well-defined binding residues at specific sequential spacing (Fig 1B, Supplementary table 2).

To gain insight into the phylogenetic distribution of MOG_{35-55} analogs derived from the human microbiome, we examined the 21,557 analogs with well-defined binding motifs. Those analogs exhibited a wide distribution across 24 phyla, with the

occurrence of a specific motif per genome varying from 0 to 1 within each phylum (Fig 1C). Of note, 10 phyla with fewer than 10 genomes and 19 unclassified bacteria-derived contigs at the phylum level were grouped as “Others”. Interestingly, Verrucomicrobiota demonstrated a higher likelihood of encoding analogs featuring the YRxxFxRVx motif. Besides, these analogs were predominantly encoded by species such as *A. muciniphila* or *A. muciniphila.B*, which are enriched in patients with MS (24).

Microbiome-derived peptide-MHC II-TCR complexes structure-prediction

Following the general model of antigen presentation (25, 26), we employed a fine-tuned AlphaFold with a binding classifier (27) to discriminate ligands with mouse MHC II molecules (H2-Ab) binding core peptides. Subsequently, the binding core peptides were subjected to modeling the peptide-MHC II-TCR complex by TCRdock (28). First, the performance of fine-tuned AlphaFold and TCRdock was assessed using the MOG_{35-55} peptide as a test case (Fig 2). MOG_{35-55} peptide was further chopped into 10 unique putative binding core peptide candidates (Fig 2A) for subsequent analyses. This was necessary because the current state-of-the-art machine learning-based structure predictors (27-30) for the peptide-MHC II-TCR complex are designed to predict binding between a 9-mer binding core peptide and its receptor (MHC II or TCR). Finally, the binding core peptide of MOG_{35-55}, with the specific sequence "WYRPPFSRVVH", was predicted to be MHC II binders (Fig 2A),

and this binding core peptide exhibited reliable interactions with four TCRs that contained different gene segments (Fig 2B). It is noteworthy that this binding core peptide with the sequence “WYRPPFSRVVH” could interact with mouse MHC II and TCR is consistent with the previous studies (20, 31). Inspired by these results, we integrated these two methods to prioritize the microbiome-derived epitopes.

To mimic the process of proteolytical degradation of exogenous proteins before their presentation to MHC II in antigen presentation (26), we truncated the corresponding peptide windows (~ 21 residues) containing the binding motifs along these 3,946 analogs, resulting in 731 nonredundant putative ligand sequences (Fig 3A, Supplementary table 2, 3). These ligands were further chopped into 5,783 unique putative binding core peptide candidates (Supplementary table 3) for subsequent analyses. Consequently, we identified 493 binding core peptides from 439 ligands as MHC II binders (Fig 3B, Supplementary table 4). In addition, we successfully modeled interactions between peptide-MHC II and 4 types of TCRs for 97.8% of the MHC II binders using 4 peptide-MHC-TCR complexes templates (Supplementary Fig 1 and Fig 2, Supplementary table 4). To determine the binding specificity, binding motifs are generated from these binding core peptides and characterized by anchor positions (Fig 3C and 3D). The motifs revealed that Y/F, R, F, R, and V residues are enriched at well-defined anchor positions (loc_1, loc_2, loc_5, loc_7, loc_8) in this study. Surprisingly, several noncanonical binding motifs starting with “L”, “A”, “I”, “S”, “N”, “H”, “Q”, “V”, “T”, “M”, “W”, and others were also observed (Fig

3C). These findings suggest that microbiome-derived epitopes could interact with MHC II and TCRs with diverse binding characteristics.

Microbiome-derived peptide stimulates MOG_{35-55}-specific T cell

In order to investigate the potential modulatory effects of microbiome-derived peptides resembling MOG_{35-55} peptide sequence on the autoimmune response that triggers EAE, a total of 8 peptides (Fig 3 and 4A) were selected from a pool of 439 ligands. These 8 peptides were confidently modeled in pMHC II-TCR interactions (Fig 3), and their selection was based on four specific criteria. Firstly, ligands that contained the "YRxxFxRVx" motif were considered. Secondly, ligands that could be detected in the NBDC database were included (specifically, P1, P2, P4, P5, P6, and P8). Thirdly, ligands collected from species related to MS were chosen (P3 and P5) (24). Finally, ligands containing noncanonical binding motifs starting with "F" and "L" were selected (P1, P3, P7, and P8), as these motifs were found to be most enriched in the pool of 493 binding core peptides. To investigate the potential of microbe-derived peptides to activate MOG_{35-55}-specific T cell, we stimulated splenocytes isolated from MOG_{35-55}-induced EAE mice with MOG_{35-55} peptide and 8 selected peptides (Fig 4A). Of the tested 8 microbiome-derived peptides, P3 demonstrated the capacity to stimulate the production of IL-17 and IFN-γ by MOG_{35-55}-specific T cells (Fig 4B-D, supplementary Fig 3A). It is noteworthy that P3 was identified as originating from *A. muciniphila*, a gut commensal that is significantly enriched in the

gut microbiota of individuals with MS (5).

P3 exacerbate EAE development in mice and shows bidirectional cross reactivity with MOG_{35-55} peptide *in vitro*

To further explore the impact of microbiome-derived peptide on EAE development, C57BL/6J mice were immunized with a combination of P3 and a low dose of MOG_{35-55}. We found that P3 could exacerbate EAE development in mice (Fig 5A). At 17 days post-immunization, the spinal cord tissues were collected, and flow cytometry as well as Hematoxylin and Eosin (H&E) or Luxol Fast Blue (LFB) staining were performed to determine the impact of P3 on the severity of inflammation and demyelination. As shown in Fig 5B, increased leukocyte infiltration was observed in the MOG_{35-55} + P3 group, implicating more severe immune infiltration in this group. Moreover, more severe inflammation was observed in the white matter of spinal cord from mice immunized with P3 and MOG_{35-55} compared to the control mice (Fig 5C). Quantitative analysis revealed that the inflammatory scores (H&E score) in the MOG_{35-55} + P3 group were significantly higher than the MOG_{35-55} + control group (Fig. 5C). Additionally, the demyelination level (LFB score) showed an increasing trend in mice immunized with MOG_{35-55} + P3 compared to the control mice (Fig. 5D).

Splenocytes from P3 immunized mice (10-day post-immunization) were collected to further test the cross-reactivity between P3 and MOG_{35-55}. Following an 18-hour stimulation of P3-specific $CD4^+$ T cells either with P3 or MOG_{35-55}, the cells exhibited

a robust immune response to P3 and a relatively strong response to MOG_{35-55} as indicated by the production of IFN-γ (Fig 6). These data suggest that the microbial peptide P3 and MOG_{35-55} can stimulate a bidirectional cross-reactive immune response.

DCs process microbiome-derived peptide P3 and further activate 2D2 $CD4^+$ T cell proliferation

Given that P3 stimulated MOG_{35-55}-specific $CD4^+$ T cells *in vitro*, we investigated whether DCs are capable of processing and presenting P3 to MOG_{35-55}-specific T cells. Our pMHC II-TCR model predicted an interaction between the 11- residue windows with the core 9-mer residues truncated from microbiome-derived peptide and the MHC II-TCR complex (Fig 7A and 7B), leading us to hypothesize that this peptide could be presented by DCs. To test this hypothesis, we performed an antigen presentation assay using DCs isolated from the spleens of C57BL/6J mice. The DCs were primed with either PBS, P3, or MOG_{35-55}, and then co-cultured with sorted 2D2 $CD4^+$ T cells. The activation status of $CD4^+$ T cells was later assessed by quantifying the expression of the early T cell activation marker CD69. Furthermore, the proliferation of $CD4^+$ T cells was evaluated by monitoring the changes in the population of CFSE-labeled cells. The results demonstrated that P3 could be presented by DCs and subsequently activate the proliferation of 2D2 $CD4^+$ T cells (Fig 7C). However, P3 induces a weaker $CD4^+$ T cell activation and

proliferation than MOG_{35-55} (Fig 7D), which may explain the lower incidence and clinical score observed in P3-induced EAE (Supplementary Fig 4).

Discussion

The gut microbiota has been implicated in the development of autoimmune diseases. Investigations of MS patients and the EAE mouse model have revealed that the gut microbiome is a crucial factor in disease progression and severity (4, 5). Alterations in gut bacterial composition, including reductions in butyrate-producing bacteria and increases in *Akkermansia* and *Clostridia* populations have been consistently observed in MS patients (5, 7). Moreover, transfer of microbiota from MS patients to animal models has been shown to increase disease incidence, suggesting that alterations in the microbiome may actively contribute to the development of MS (32). Germ-free and antibiotic-treated mice have shown resistant to EAE, further supporting the necessity of the microbiome for disease induction (33, 34).

Despite significant advances in understanding the role of the gut microbiota in MS pathogenesis, the underlying mechanisms leading to disease development remain poorly understood. Continuous sampling of gut microbial antigens by innate immune cells enhances the probability of presenting specific antigens to antigen-specific T cells. The presentation of these antigens is influenced by polymorphisms in MHC genes, suggesting a potential role for host-commensal microorganisms cross-

reactivity in the development and persistence of autoimmunity among genetically predisposed individuals. Molecular mimicry has been proposed as a possible mechanism by which microorganisms can induce autoimmune diseases (15). According to this hypothesis, T cells that respond to an epitope derived from an infectious agent may cross-react with a self-antigen that share sequence or structural similarities with the original microbial peptide (35). Evidence supporting this hypothesis has been observed in numerous autoimmune diseases, such as antiphospholipid syndrome and Type 1 Diabetes (36, 37). Given the diverse range of microorganisms in the gut, peptides derived from gut flora could potentially trigger the development of MS. The activation of autoreactive T cells is a critical component of the early autoimmune response in individuals who ultimately develop MS. While multiple potential antigens exist, MOG is a major EAE antigen in H-2b mice and a possible autoantigen in MS (20). The binding pattern of the MOG-MHC II-TCR complex has been characterized, revealing that tyrosine (Y) in position 40 of the MOG_{35-55} peptide is the dominant MHC II-binding residue, occupying the p1 pocket. Meanwhile, arginine (R) 41, phenylalanine (F) 44, R46, and valine (V) 47 are the major amino acids involved in TCR recognition (20). Research suggests that low-affinity hotspot mimicry, which involves a subset of crucial residues within the TCR-binding footprint, rather than high-affinity structural mimicry, may be a more common contributor to the initiation of autoimmune diseases (14, 20). In our study, we focused on identifying MOG_{35-55} mimics based on the similarity of essential

residues within the TCR-binding footprint, rather than relying on the direct amino acid similarity between microbial-derived peptides and self-antigens, as reported in studies on Type 1 Diabetes (37).

By leveraging the expanding genome databases for human gut microbes, we identified 8 microbial peptides that exhibit significant analogy in their antigen-MHC II-TCR binding patterns with MOG_{35-55} peptide. Our findings indicated that microbiome derived P3 can activate $CD4^+$ T cells specific to MOG_{35-55} peptide in mice. Interestingly, our bioinformatic analysis revealed that this peptide was derived from *A. muciniphila*, suggesting a potential impact of *A. muciniphila* on EAE development. Previous studies have explored the link between *A. muciniphila* and EAE or MS, such as the findings of Cekanaviciute *et al*., who observed that *A. muciniphila* promotes Th1 differentiation in human peripheral blood mononuclear cells (5). Moreover, previous studies have demonstrated that a peptide from *A. muciniphila* shares a similar sequence with a MS associated self-antigen, guanosine diphosphate (GDP)–L-fucose synthase. This shared peptide sequence has the ability to stimulate the proliferation of $CD4^+$ cerebrospinal fluid-infiltrating T cells from MS patients (16).

In this study, we optimized the process of screening self-antigen mimics from gut microbiota by integrating the binding affinity to MHC II and TCR into the selection criteria, thereby enhancing the accuracy of identifying self-antigen analogs in the gut

microbiome. Furthermore, our findings suggest that the enrichment of *A. muciniphila* in the gut microbiota of EAE mice and MS patients may have pathological implications as this bacterium has the capability of generating MOG_{35-55} analogs. However, our method utilizing metagenomic data can only annotate genome to species level, and further determination is needed to identify the specific *A. muciniphila* strain capable of producing MOG_{35-55} analogs.

A. muciniphila, a next-generation probiotic, has shown positive effects on several diseases including obesity and diabetes (38). However, recent studies have revealed an enrichment of *A. muciniphila* in the gut microbiome of MS patients. Furthermore, transplantation of fecal samples from MS patients into the intestines of EAE mice leads to more severe EAE symptoms (5), indicating the need to assess the potential beneficial or harmful effects of *A. muciniphila* from multiple perspectives. Although multiple strains of *A. muciniphila* have been identified (39), it remains unclear whether the observed effects in different disease contexts are attributable to strain differences. The predominant use of metagenomics and 16S sequencing in numerous studies exploring the relationship between various diseases and *A. muciniphila* has impeded the identification of specific target strains, as these methods primarily facilitate gene annotation at the species level, presenting challenges in strain-level identification. Our study suggests that *A. muciniphila* may contribute to the development of EAE due to its capacity to generate MOG_{35-55}-resembling peptides. However, more evidence are needed to

determine the target strain that generates MOG_{35-55} analogs. Future studies will also focus on elucidating the role of synergistic or antagonistic effect among different microbial populations in autoimmune diseases. This study highlights the necessity for further research on the correlation between gut microbiota and autoimmune diseases in the growing trend of widespread probiotic consumption.

In summary, our findings prove a mechanism of molecular mimicry in which a particular sequence within commensal gut microbe can imitate crucial residues in the MOG-MHC II-TCR binding footprint, consequently initiating or modifying the immune response associated with EAE development. While our study focused only on MOG_{35-55} mimics, other myelin antigens, such as MBP and PLP, may also serve as targets for autoreactive $CD4^+$ T cells (40). Given the enormous number of microbial peptides generated by the gut microbiota, it is possible that other microbial peptides may exist and can mimic these antigens and activate related autoantigen reactive T cells. Meanwhile, it's important to note that the induction of autoimmune diseases through molecular mimicry is complicated and a single factor acting alone is unlikely to trigger the disease. Instead, accompanying host genetic susceptibility is considered to be linked with an abnormal immune response triggered by one or more microbial antigens or molecules. Nonetheless, this discovery may provide a therapeutic target and an opportunity to impede the progression of MS.

Conclusion

We have investigated the role of molecular mimicry in the link between microbial flora and EAE development. We have identified MOG_{35-55} mimics derived from gut commensal cross-react with MOG_{35-55}-specific $CD4^+$ T cells and significantly exacerbate the development of EAE in mice. Notably, antigen-presenting assays confirmed that DCs can process and present this gut commensal derived peptide to MOG_{35-55}-specific $CD4^+$ T cells. Our findings offer direct evidence of how microbes can initiate the development of EAE, suggesting a potential microbiome-based therapeutic target for inhibiting the progression of MS.

Material and Methods

Identify the human MOG_{35-55} peptide analog in the human microbiome genomes and human-associated metagenomic samples

In brief, we first collected and curated human microbiome-derived peptide resources, which included human microbiome genomes and human-associated metagenomics samples. In detail, we collected 286,997 human microbiome genomes from Unified Human Gastrointestinal Genome dataset (UHGG, v1.0) (41), and 17249 genomes from CIBIO species-level genome bins (21). Taxonomic assignments were performed for genomes from CIBIO by GTDB-tk (42). In addition, we downloaded 103 metagenomes from MS patients in National Bioscience Database Center (NBDC) Human Database with the accession number of hum0197 (43). The data obtained from the UHGG and NBDC were acquired in accordance with human

research ethics guidelines and were approved by the Human Ethics sub-Committee of the City University of Hong Kong (jcc2223ay001). For these metagenomic samples, we applied metagenomic assembly to obtain contigs using MEGAHIT (44) for each sample separately. Taxonomic classification was further conducted for the resulting contigs using CAT (v5.2.3) (45). Taxonomic assignments for genomes or contigs based on the Genome Taxonomy Database (46). Finally, all open reading frames were predicted in each genome or contig using Prodigal-short (47). Human MOG_{35-55} sequence analog searching was conducted by BLASTp with an e-value threshold of 0.001 in a pool of proteins from the above Human microbiome-derived peptide resources.

The structure-based prediction of peptide-MHC II-TCR binding

Identified analogs were first filtered based on whether they contained the motifs with [YR..F.RV.], [YR..F.R..], [YR..F..V.], [YR....RV], and [Y...F.RV.] are involved in the peptide-MHC-TCR interactions. Next, a special peptide region (~ 21 residues) containing the above binding pattern was truncated from these filtered analogs. The yielded nonredundant truncated peptides were subjected to further analyses.

The peptide-MHC II-TCR binding prediction was performed in two steps: the peptide-MHC II binding specificity prediction and TCR: peptide-MHC II interactions modeling. Because the advanced peptide-MHC II structure prediction tools often predict the binding structure composed by the binding core of peptides (normally

with 9 residues) and receptors (MHC II or TCR) (27-30, 48), these nonredundant truncated peptides were further chopped into a series of consecutive 11-residue windows along peptide with the putative core nine-mer residues and their immediate neighboring residues. The resulting 11-residue windows were subjected to a fine-tuned AlphaFold to predict peptide-MHC II binding with the following parameters: --model_names model_2_ptm_ft --ignore_identities (27). Peptide-MHC II templates (4p23_MH2_H2ABa_H2ABb.pdb,6mng_MH2_H2ABa_H2ABb.pdb,1muj_MH2_H2ABa_H2ABb.pdb) in the PDB template set were used (27). Mean Inter-chain lowest predicted aligned error (PAE) terms corresponding to the peptide-MHC interactions ≤ 4.34 and peptides' per-residue confidence score (pLDDT) corresponding to local structural accuracy ≥ 90 were used to classify MHC II binder and non-binder. Next, peptide-MHC II-TCR binding for the predicted binders was modeled by a specialized version of the neural network predictor AlphaFold and TCR–pMHC complex templates-based method, TCRDock with 'model_2_ptm' and '--benchmark' parameter set (28). Based on TCRDock's workflow, three simulations were conducted for each target peptide-MHC II-TCR complex, and finally chose the model with the lowest PAE between the TCR and pMHC. Given the hypervariable gene segments in TCR alpha and beta chain largely determine the structure modeling (49), we took TCR:pMHC II structural templates (PDB IDs: 3c60, 3rdt, 3c5z, 6mnn), pairing with four types of mouse TCR (Supplementary table 5), to model the peptide-MHC II-TCR structures. The predicted structures were visualized

by PyMoL.

Mice

Eight-week-old C57BL/6J mice were obtained from the Laboratory Animal Research Unit (LARU) of City University of Hong Kong. The 2D2 TCR transgenic mice C57BL/6-Tg (Tcra2D2, Tcrb2D2) 1Kuch/J were purchased from The Jackson Laboratory and bred in LARU. Mice were randomly allocated to each treatment group. All experimental procedures were approved by the Animal Ethics Committee of the City University of Hong Kong and performed in accordance with LARU Guidelines.

EAE induction

For induction of active EAE, mice (8-week-old) were immunized subcutaneously at two sites on the back flank area with 200 μg of $MOG_{35–55}$ (MEVGWYRSPFSRVVHLYRNGK) peptide (Thermo Fisher) emulsified in 200 μl incomplete Freund's adjuvant (BD bioscience) supplemented with 2 mg/ml heat-killed *Mycobacterium tuberculosis* (BD bioscience). On days 0 and 2 after immunization, mice received intraperitoneal 400 ng of pertussis toxin (Calbiochem). The same immunization procedure was employed to detect the encephalitogenic capacity of P3, using a combination of P3 and $MOG_{35–55}$ (P3: 200 μg; $MOG_{35–55}$: 50μg;). The other group was administered same dose of a combination of irrelevant peptide (set as a control of P3) and $MOG_{35–55}$. EAE severity was scored daily using

the standard scale: 0, no disease; 1, loss of tail tone; 2, hind limb weakness; 3, hind limb paralysis; 4, hind limb paralysis and forelimb paralysis or weakness; and 5, moribund/death (50). To detect the cross reactivity between MOG_{35-55} and synthesized peptides, mice were injected with peptide by following the similar immunization procedure (DG peptides, China). The same immunization protocol was employed to induce EAE using P3.

Antigen recall assay

T cell antigen recall response was assessed in cells harvested from the spleen of EAE mice 10 days after the challenge. Mice were anesthetized by 3% isoflurane inhalation and then euthanized by cervical dislocation. Spleens were then collected from the euthanized mice and crushed through a 70-μm cell strainer and centrifuged at 400 × g for 5 min at 4 °C, then incubated in red blood cell lysis buffer (Thermo Fisher) for 5 min. After centrifuge, isolated cells were plated at a density of $1x10^6$ cells/well and stimulated with synthesized peptide or $MOG_{35–55}$ (20 μg/ml final concentrations) in cell culture media (RPMI1640, 10% FBS, 2 mM L-glutamine, 10 mM Hepes, 50 μM 2-mercaptoethanol, 100 IU penicillin, and 100 μg/mL streptomycin), in a total volume of 200 μL per well. Cells were stimulated for 18h at 37 °C and 5% CO_2 atmosphere, then analyzed by flow cytometry for cytokine (IFN-γ, IL-17A) producing cells.

Histopathology

Inflammation and demyelination of spinal cords was assessed at day 17 after immunization. The lumbar enlargement of the spinal cords was isolated from animals and instantly fixed in 4% paraformaldehyde for a minimum of 48 h, then embedded in paraffin and sectioned at 5-μm thickness. Sections were stained with H&E (Solarbio) or LFB (Abcam) to evaluate inflammation and demyelination. The sections were scanned using a NanoZoomer S60 Digital slide scanner (Hamamatsu). The degrees of inflammation (H&E scores) were calculated as 0, normal; 1, cellular infiltrates partially around meninges and blood vessels; 2, 1–10 lymphocyte infiltrates in the parenchyma; 3, 11–100 lymphocyte infiltrates in the spinal cord; 4, 100-300 lymphocyte infiltrates in the spinal cord; 5, 300-1000 lymphocyte infiltrates in the spinal cord; and 6, over 1000 lymphocyte infiltrates in the spinal cord (51). The severity of demyelination (LFB scores) was analyzed as 0, normal; 1, myelin sheath injuries in rare areas; 2, a few areas of demyelination; 3, confluent perivascular or subpial demyelination; 4, massive demyelination involving one half of the spinal cord; and 5, extensive demyelination involving the whole spinal cord (51).

Antigen presentation assays

To obtain stimulator DCs, single cell suspensions from the spleen collected from C57BL/6J mice were prepared by mechanical disruption on a 70-μm cell strainer. Cell suspensions were resuspended in MACS buffer (0.5% BSA, 2 mM EDTA in

PBS) after lysing red blood cells. $CD11c^+$ cells were then negatively selected according to the manufacturer's instructions using the mouse Pan Dendritic Cell Isolation Kit (Miltenyitec). Isolated DCs were pulsed with either PBS, P3, or MOG_{35-55} at 20 µg/ml final concentrations, using 2 x 10^4 cells in 96-well plate for 1 h at 37 °C. Cells were then washed extensively and used for co-culture with responder 2D2 $CD4^+$ T cells. Responder MOG_{35-55}-specific $CD4^+$ T cells were isolated from 2D2 TCR transgenic mice spleen by using $CD4^+$ T cells Isolation Kit (Miltenyitec). Sorted $CD4^+$ T cells were labeled with Carboxyfluorescein succinimidyl ester (CFSE, Thermo Fisher) following the user guide. 10^5 CFSE labeled 2D2 $CD4^+$ T cells were then seeded in triplicate in a round bottom 96-well plate with 2 x 10^4 stimulated DCs (5:1 ratio). DCs and T cells were cultured together for 72 h at 37 °C and 5% CO_2 atmosphere, then cells were prepared for flow cytometry to detect T cell proliferation.

Flow cytometry

Single cell suspensions from the spleen were obtained by mechanical disruption on a 70-µm cell strainer, then incubated in red blood cell lysis buffer for 5 min. For the staining process, dead cells were stained with Propidium Iodide (Sigma-Aldrich) or Live/Dead Ghost dye (Tonbo Biosciences). For staining of surface markers, cells were incubated in fluorescently labeled antibodies (CD45, CD3, CD4, CD69, TCR $V_\beta11$) for 30 min in FACS buffer (PBS containing 2% FBS) at 4 °C. For intracellular staining, cells were washed with 2 mL wash buffer, then fixed and permeabilized by

using Cytofix/Cytoperm™ Fixation/Permeabilization Kit (BD Biosciences) as manufacturer's instructions. Fixed cells were incubated in fluorescently labeled antibodies (IFN-γ, IL-17A) for 30 min in permeabilization buffer at 4 °C. All data were collected on a BD Celesta flow cytometer (BD Biosciences) and analyzed using FlowJo software (v.10.2, BD Biosciences).

Statistical analysis

Data were analyzed using GraphPad Prism software and reported as mean ± SEM unless otherwise noted. The two-tailed unpaired Student *t test* was used for samples with equal variances, whereas Welch's *t test* was employed for samples with unequal variances. Statistical significance was defined as a *p*-value <0.05.

Abbreviations

MS: Multiple sclerosis

MOG: Myelin oligodendrocyte glycoprotein

MOG_{35-55}: Myelin oligodendrocyte glycoprotein peptide 35-55

EAE: Experimental autoimmune encephalomyelitis

DCs: Dendritic cells

A. muciniphila: Akkermansia muciniphila

MBP: Myelin basic protein

PLP: Proteolipid protein

UHGG: Unified Human Gastrointestinal Genome dataset

NBDC: National Bioscience Database Center

PAE: Predicted aligned error

pLDDT: Peptides' per-residue confidence score

Hematoxylin and Eosin: H&E

Luxol Fast Blue: LFB

Declarations

Ethics approval and consent to participate: The data obtained from the UHGG and NBDC were acquired in accordance with human research ethics guidelines and were approved by the Human Ethics sub-Committee of the City University of Hong Kong (jcc2223ay001). And all experimental procedures were approved by the Animal Ethics Committee of the City University of Hong Kong and performed in accordance with LARU Guidelines.

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Reference

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Figure legends

Figure 1. Overview of MOG_{35-55} analogs identified in the human microbiome.

(A) The workflow of human microbiome-derived peptides discovery. (B) The proportion of MOG_{35-55} analogs with well-defined binding motifs. (C) Chord diagram

showing the taxonomy distribution of prioritized analogs. The values in brackets show the total number of analogs with corresponding binding motifs. per genome in each phylum. The counts of analogs in each phylum were normalized by the genome counts. The scale was the proportion of analogs in each motif (upper) or in each phylum. Of note, the genomes less than 10 counts from *Firmicutes_I*, *Firmicutes_B*, *Bacillota_B*, *Cyanobacteria*, *Desulfobacterota_I*, *Fusobacteriota*, *Pseudomonadota*, *Euryarchaeota*, *Halobacterota*, *Patescibacteria*, and 19 unclassified contigs were merged into Others.

Figure 2. The confidence of $hMOG_{35-55}$ binding core peptide-MHC II and peptide-MHC II-TCR complexes predicted TCRDock.

The scatter plots show the pLDDT value of a peptide versus an averaged inter-chain PAE of peptide-MHC-II complexes (A) and peptide-MHC II-TCR complexes (B) for binding core peptide candidates chopped from human MOG_{35-55}. The predicted MHC II binding peptides (pLDDT ≥ 90, inter-PAE ≤ 4.34) are highlighted in red. The sequence of binding core peptide candidates is listed on the right side of panel A. The modeling of a peptide with pLDDT≥ 70 is considered as confident.

Figure 3. Polymorphism in 9-mer binding core peptides of the predicted peptide-MHC II complex.

(A) The stacked bar plot shows the number of nonredundant ligands with 11 amino acids residues truncated from analogs, colored with different motifs. (B) The scatter

plot shows the pLDDT value of a binding core peptide (corresponding to local structural accuracy) versus an averaged MHC II-peptide complex's inter-chain PAE score (corresponding to the peptide-MHC II interactions). The predicted binder is highlighted in red. (C) The frequencies of amino acid residues (rows) at specific positions (columns) among the predicted MHC II binding peptides. The loc_1 ~ loc_9 represent the binding core region among the binder, and loc_0 and loc_10 represent the flanking region of binders. (D) Representative sequence logos illustrating peptide residue preference of MHC II. Each logo is labeled with the starting amino acid residue of binding core peptides, and the number of binding core peptides used to generate the logos is paired to the corresponding cells in panel [B]. The logos are colored by the chemical polarity of the amino acid residue. In panels C and D, sequence/residue numbers are 0-indexed: they start at 0 and end with N-1, where N is the length of the sequence.

Figure 4. Microbiome-derived peptide can stimulate MOG_{35-55}-specific T cells from EAE mice.

(A) The origin and sequence of microbial peptides tested in this study. The amino acids highlighted in green are the dominant MHC II-binding residue, while major TCR contact residues are colored in red. The amino acids colored in blue represent different residue between human MOG_{35-55} and mouse MOG_{35-55}. The asterisk highlights that P5 is a peptide predicted in both *Alistipes putredinis* and *A.*

692 *muciniphila*. (B, C and D) MOG_{35-55}–specific $CD4^+$ T cells collected from the spleen
693 of EAE mice were treated with each of the selected 8 microbial peptides. PBS and
694 MOG_{35-55} served as negative control and positive control; Irrelevant peptide was set
695 as scrambled peptide control. Flow cytometry was used to determine IFN-γ and IL-
696 17 production (n = 3). Representative FACS plots (gated on $CD3^+$ and $CD4^+$ cells)
697 for the population of IFN-γ- or IL-17-secreted $CD4^+$ T cells that were stimulated with
698 mimic peptides or MOG_{35-55} (20 μg/ml final concentration). Only data from P3, which
699 induced the highest cytokine-producing cell population was shown (B), along with
700 the frequency (C) and cell counts (D) of each population among $CD4^+$ T cells (Red
701 triangle specifically point P3 treatment group). Data shown are the average ± SEM.

702 **Figure 5. P3 immunization exacerbates EAE development *in vivo*.**
703 (A) Mean EAE clinical scores and incidence rate from each group of mice. (B)
704 Spinal cord samples were collected at day 17 post-immunization and the leukocyte
705 population within the CNS was assessed by flow cytometry. The cell count of
706 leukocytes were significantly higher in MOG_{35-55}+P3 group than MOG_{35-55}+control
707 group (n = 8). (C, D) Spinal cord tissue sections were obtained at day 17 post-
708 immunization and stained with H&E (C) or LFB (D). The inflammatory level (H&E
709 scores) and demyelination level (LFB scores) were quantified (n=4-5). Data shown
710 are the average ± SEM. *$p<0.05$.

711 **Figure 6. P3 shows bidirectional cross-reactivity with MOG_{35-55}.**

(A, B and C) Splenocytes from P3 immunized mice (n=5) were stimulated with either P3 (positive control), MOG_{35-55}, or PBS (negative control) in a concentration of 40 µg/ml to detect the cross-reactivity between P3 and MOG_{35-55}, and activation of $CD4^+$ T cells was assessed by measuring the IL-17- and IFN-γ-producing population using flow cytometry. Representative FACS plots (gated on $CD3^+$ and $CD4^+$ cells) demonstrate the population of activated $CD4^+$ T cells (A), along with the frequency (B) and cell counts (C) of IL-17^+ and INF-γ^+ population among $CD4^+$ T cells. Data shown are the average ± SEM. *$p<0.05$, **$p < 0.01$, ***$p < 0.001$.

Figure 7. P3 stimulates 2D2 $CD4^+$ T cell proliferation through DCs presentation *in vitro*.

(A) Predicted structure of peptide-MHC II-TCR complex with binding core peptide from P3. TCR alleles same from complex template 3c60 (PDB ID). Surface representation is displayed in lighter shades. (B) Close-up view of peptide-TCR interactions (upper) and peptide-MHC II (bottom) in panel D, colored amino acid residues represent the dominant MHC II-binding residue (green) and major TCR recognition residue (red). Peptide residues and TCR alpha CDR3 (orange) and TCR beta CDR3 (hot pink) residues were shown in sticks, and residues from MHC II interacting with peptide were shown in slate blue. Hydrogen bonds are highlighted in black dashed lines. (C, D) The histogram FACS plots (C) and quantification (D) of CFSE labeled 2D2 $CD4^+$ T cells proliferation, as well as the frequency of $CD69^+$

732 cells within the $CD4^+$ T cells population, following co-culture with DCs pulsed with

733 PBS, P3, or MOG_{35-55}. Dash line in histogram represents the proliferation level of

734 PBS control. Data shown are the average ± SEM. $^{**}p < 0.01$, $^{****}p < 0.0001$.

735

Figure 1

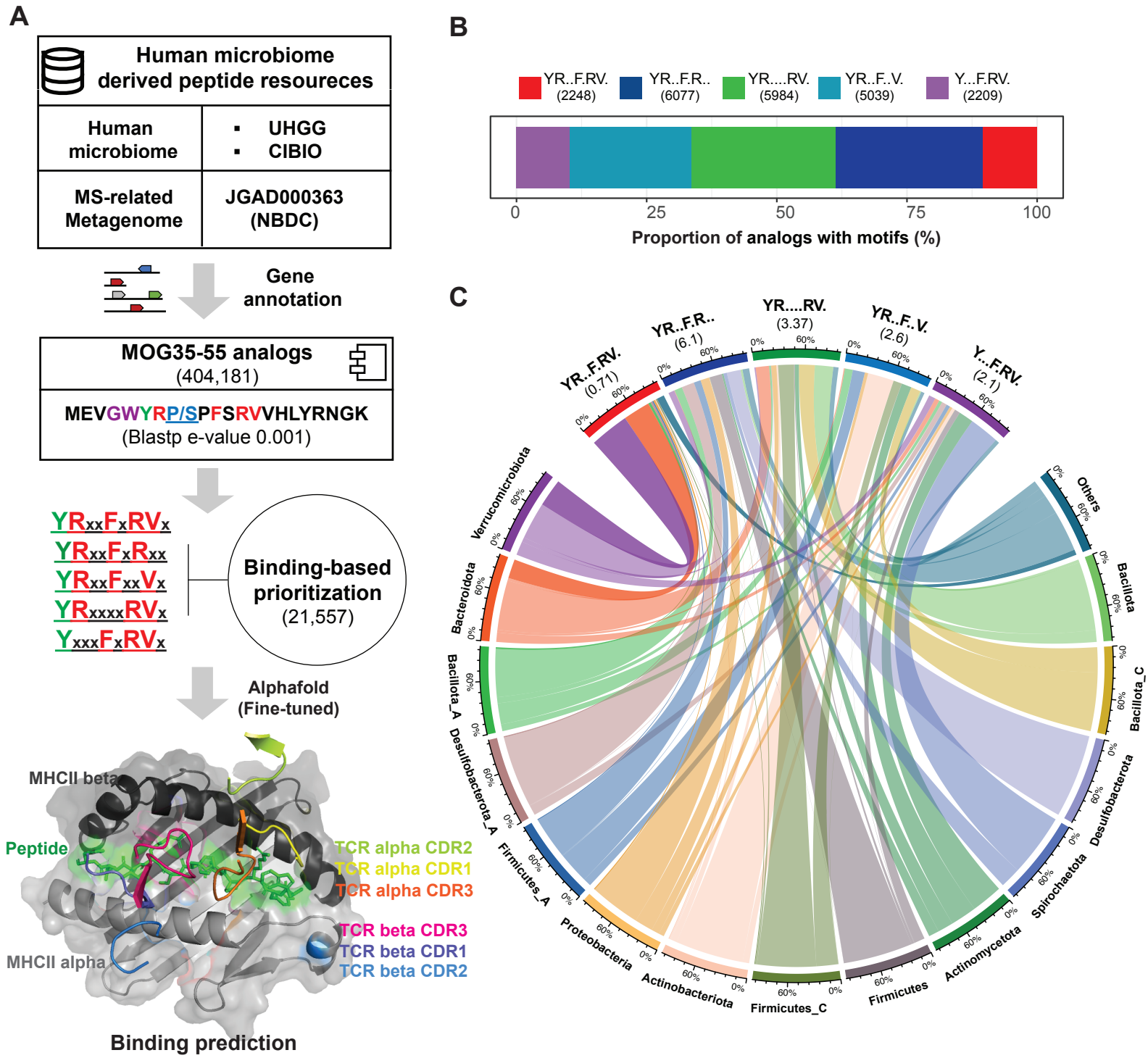

A
Human microbiome derived peptide resoureces
Human microbiome
UHGG
CIBIO
MS-related Metagenome
JGAD000363 (NBDC)
Gene annotation
MOG35-55 analogs (404,181)
MEVGWYRP/SPFSRVVHLYRNGK
(Blastp e-value 0.001)
YRxxFxRVx
YRxxFxRxx
YRxxFxxVx
YRxxxxRVx
YxxxFxRVx
Binding-based prioritization (21,557)
Alphafold (Fine-tuned)
MHCII beta
Peptide
MHCII alpha
TCR alpha CDR2
TCR alpha CDR1
TCR alpha CDR3
TCR beta CDR3
TCR beta CDR1
TCR beta CDR2
Binding prediction
B
YR..F.RV. (2248)
YR..F.R.. (6077)
YR....RV. (5984)
YR..F..V. (5039)
Y...F.RV. (2209)
0
25
50
75
100
Proportion of analogs with motifs (%)
C
YR..F.RV. (0.71)
YR..F.R.. (6.1)
YR....RV. (3.37)
YR..F..V. (2.6)
Y...F.RV. (2.1)
Verrucomicrobiota
Bacteroidota
Bacillota_A
Desulfobacterota_A
Firmicutes_A
Proteobacteria
Actinobacteriota
Firmicutes_C
Firmicutes
Actinomycetota
Spirochaetota
Desulfobacterota
Bacillota_C
Bacillota
Others

Figure 2

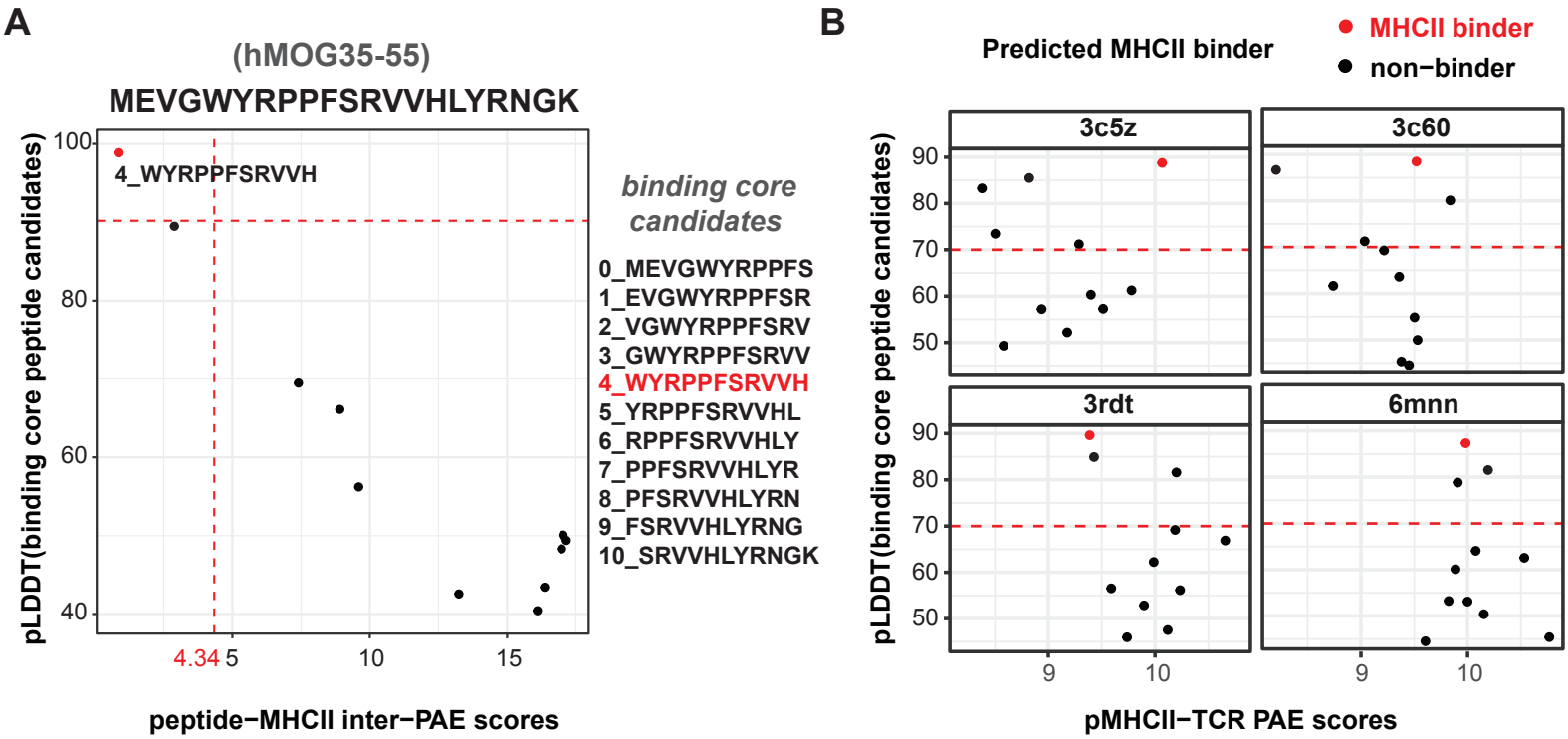

A
(hMOG35-55)
MEVGWYRPPFSRVVHLYRNGK
4_WYRPPFSRVVH
pLDDT(binding core peptide candidates)
peptide−MHCII inter−PAE scores
4.34
binding core candidates
0_MEVGWYRPPFS
1_EVGWYRPPFSR
2_VGWYRPPFSRV
3_GWYRPPFSRVV
4_WYRPPFSRVVH
5_YRPPFSRVVHL
6_RPPFSRVVHLY
7_PPFSRVVHLYR
8_PFSRVVHLYRN
9_FSRVVHLYRNG
10_SRVVHLYRNGK
B
Predicted MHCII binder
MHCII binder
non−binder
3c5z
3c60
3rdt
6mnn
pLDDT(binding core peptide candidates)
pMHCII−TCR PAE scores

Figure 3

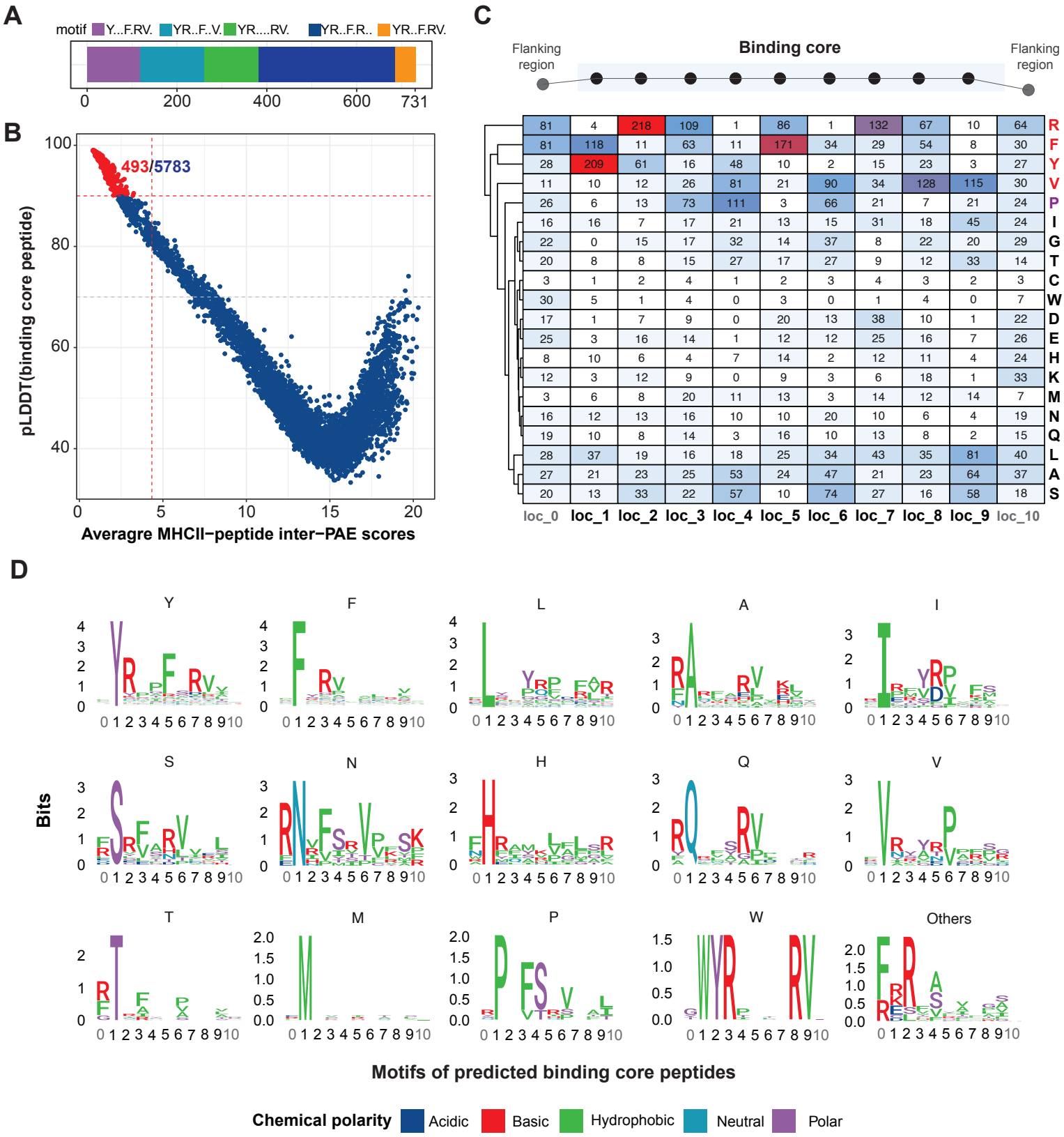
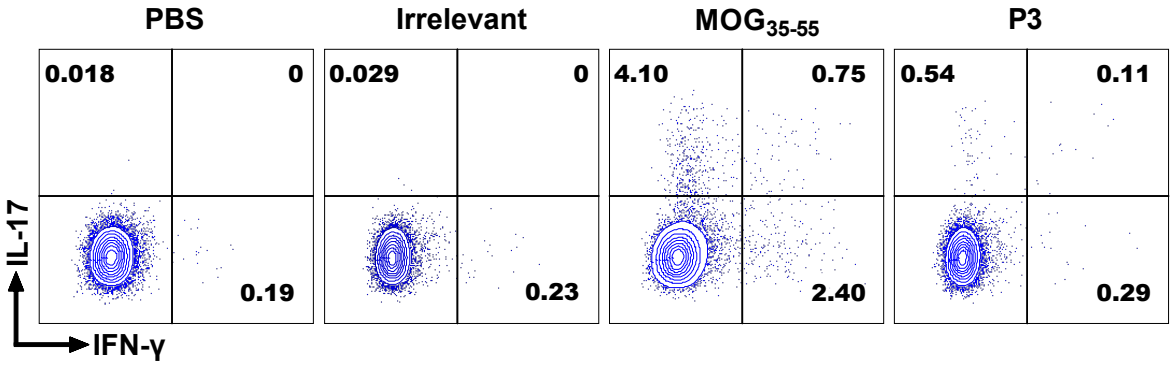

A
motif Y...F.RV. YR..F..V. YR....RV. YR..F.R.. YR..F.RV.
0 200 400 600 731
B
493/5783
pLDDT(binding core peptide)
Averagre MHCII−peptide inter−PAE scores
C
Flanking region
Binding core
Flanking region
R F Y V P I G T C W D E H K M N Q L A S
loc_0 loc_1 loc_2 loc_3 loc_4 loc_5 loc_6 loc_7 loc_8 loc_9 loc_10
D
Y F L A I S N H Q V T M P W Others
Bits
Motifs of predicted binding core peptides
Chemical polarity Acidic Basic Hydrophobic Neutral Polar

Figure 4

A

No	Taxonomy	Sequence
	Homo sapiens MOG$_{35-55}$	MEVGWYRPPFSRVVHLYRNGK
	Mus musculus MOG$_{35-55}$	MEVGWYRSPFSRVVHLYRNGK
P1	*Bacteroides* MBL fold metallo-hydrolase	PIIYFYRSAFDRVMDGVKNSK
P2	*Alistipes sp902388705*	MDVNTYRPVFLRVPMDMILK
P3	*Akkermansia muciniphila*	TTLSFYRPPFLRVRRPFYIIF
P4	*Acutalibacteraceae*_UMGS1623 sp934647945	TFVQDYRYPFLRVISLLALAA
P5	*Alistipes putredinis, Akkermansia muciniphila*	AIDWFYRRPFSRVISETVFRY*
P6	*Bacteroides caccae*	LLLLWYRKIFVRVVWLGRTRH
P7	*Angelakisella*	EELEQYRPLFGRVIIRIRTPS
P8	*Pararuminococcus gallinarum*	KLKIKYREGFFRVVHAIRDFF

B



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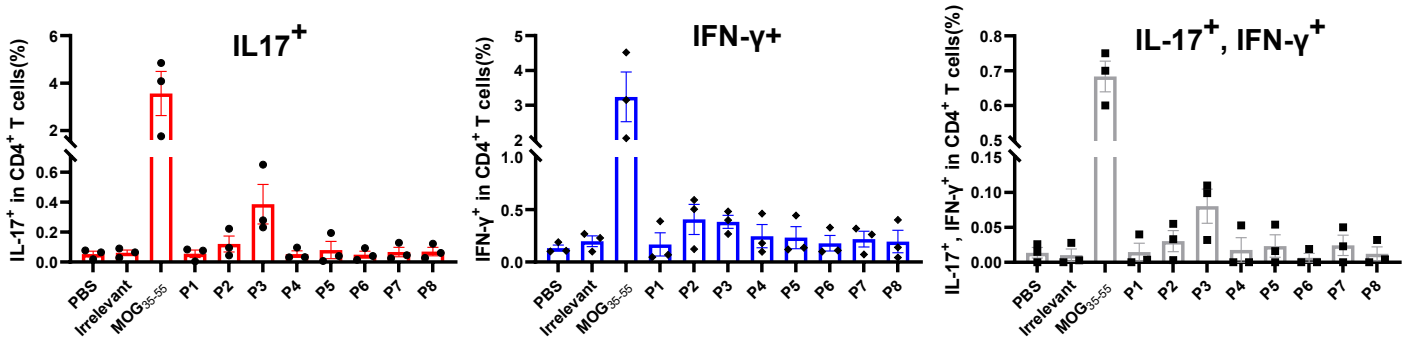

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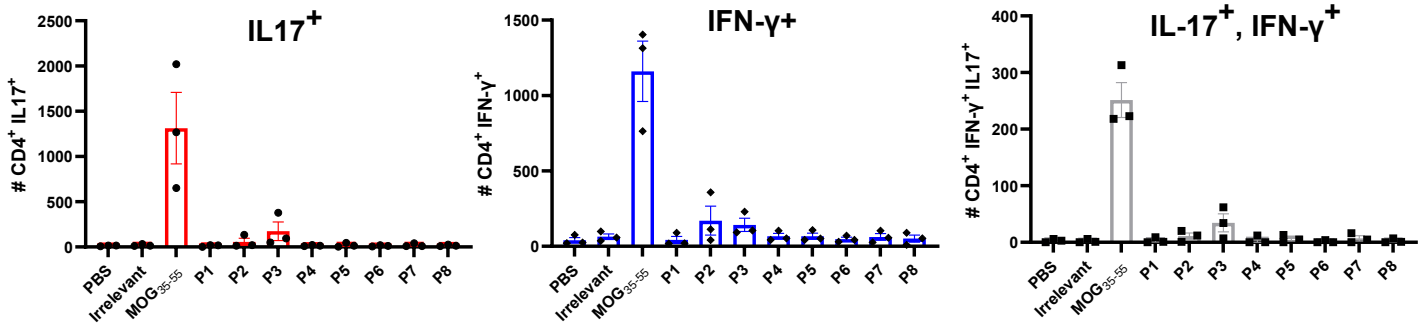


Figure 5

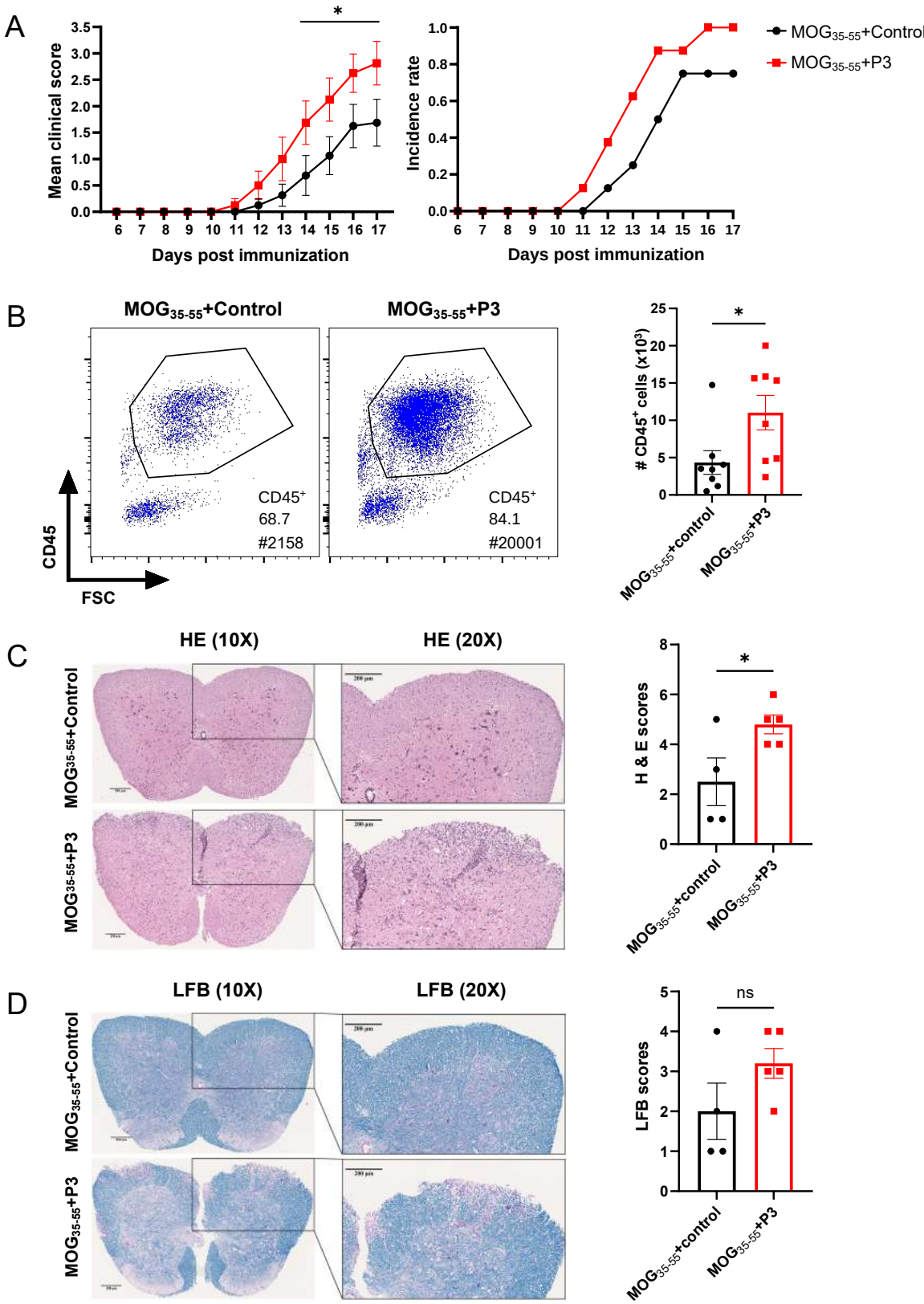

A
Mean clinical score
Days post immunization
Incidence rate
Days post immunization
MOG35-55+Control
MOG35-55+P3
B
MOG35-55+Control
MOG35-55+P3
CD45+
68.7
#2158
CD45+
84.1
#20001
CD45
FSC
CD45+ cells (x10³)
MOG35-55+control
MOG35-55+P3
C
HE (10X)
HE (20X)
MOG35-55+Control
MOG35-55+P3
H & E scores
MOG35-55+control
MOG35-55+P3
D
LFB (10X)
LFB (20X)
MOG35-55+Control
MOG35-55+P3
LFB scores
ns
MOG35-55+control
MOG35-55+P3

Figure 6

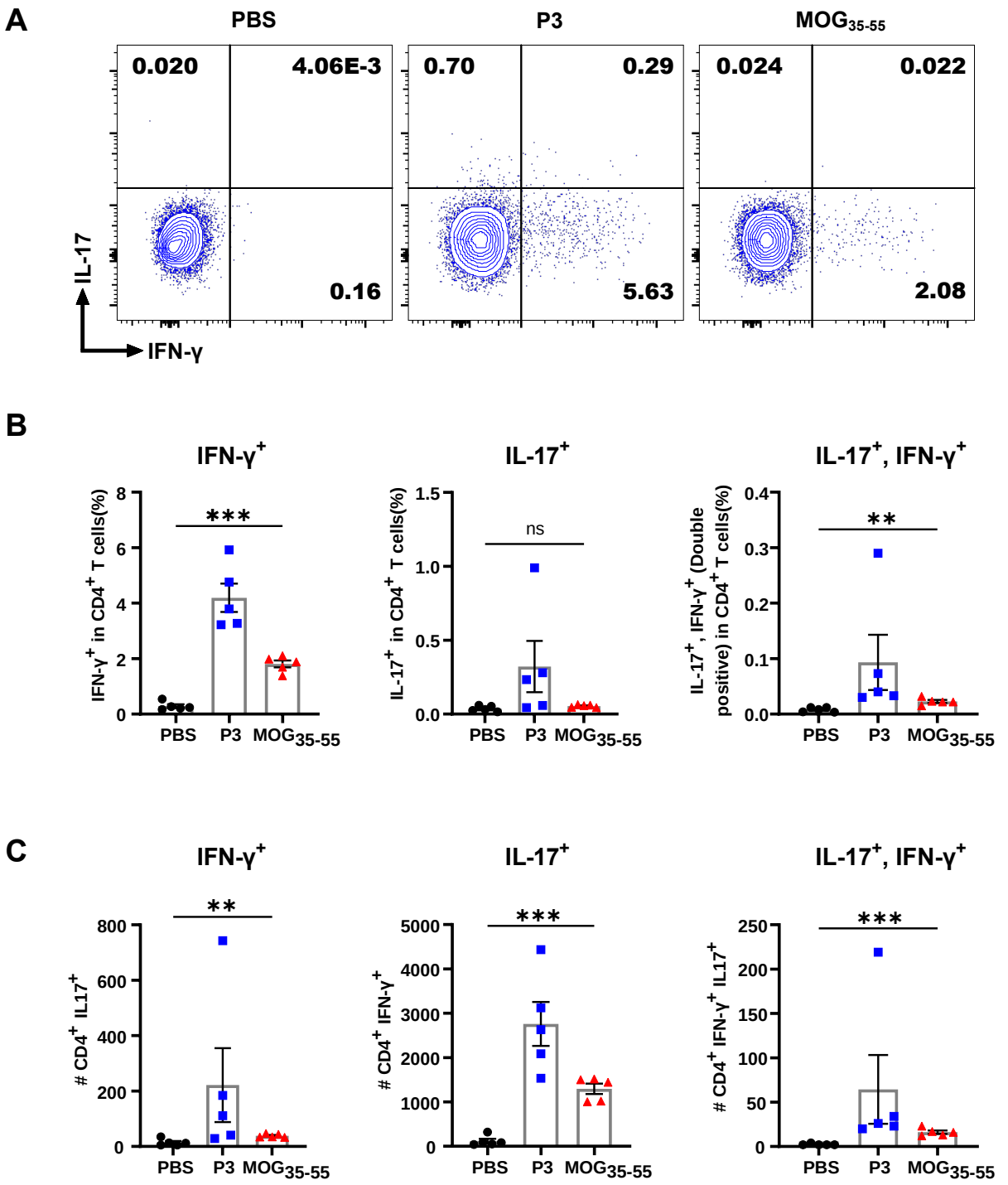
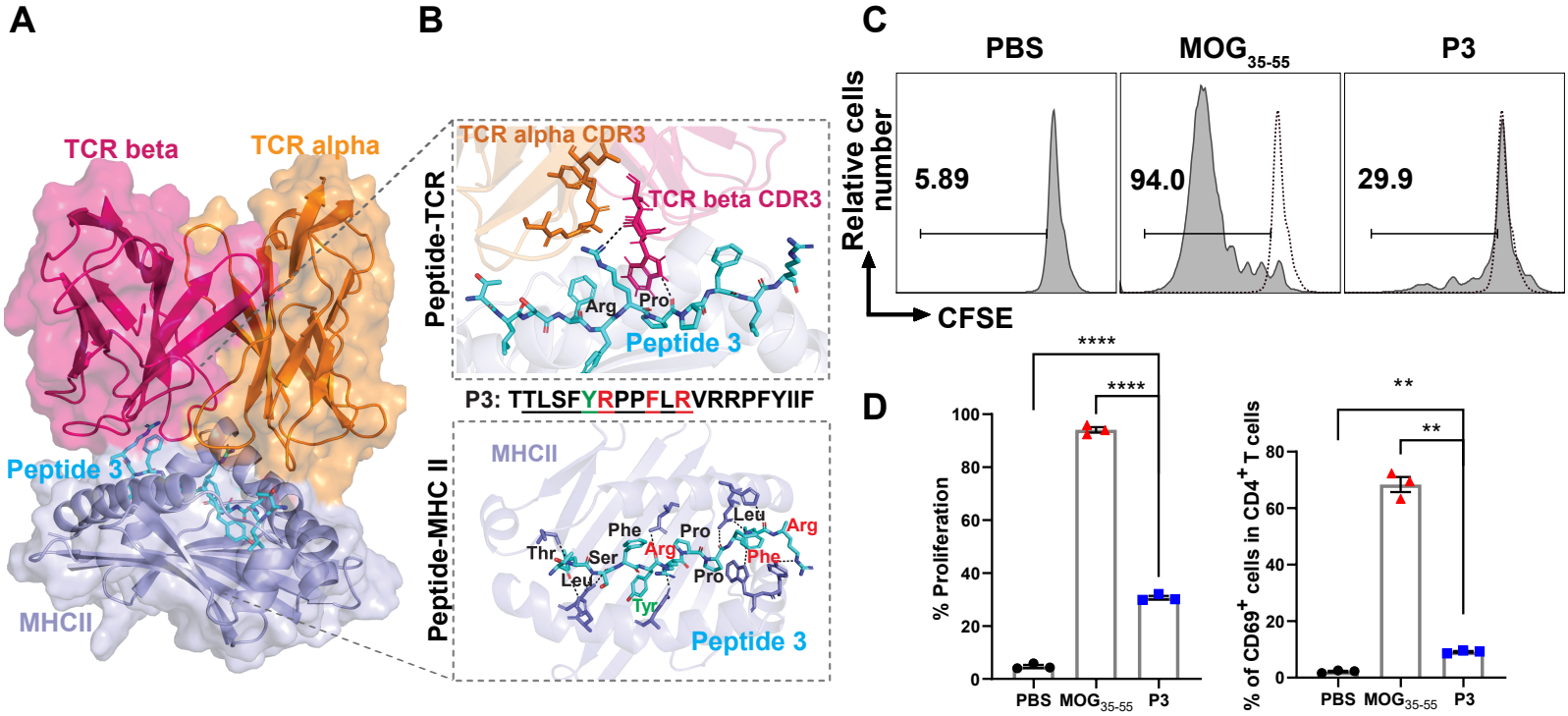

A
PBS
P3
MOG35-55
0.020
4.06E-3
0.16
0.70
0.29
5.63
0.024
0.022
2.08
IL-17
IFN-γ
B
IFN-γ+
IL-17+
IL-17+, IFN-γ+
IFN-γ+ in CD4+ T cells(%)
IL-17+ in CD4+ T cells(%)
IL-17+, IFN-γ+ (Double positive) in CD4+ T cells(%)
***
ns
**
PBS
P3
MOG35-55
C
IFN-γ+
IL-17+
IL-17+, IFN-γ+
CD4+ IL17+
CD4+ IFN-γ+
CD4+ IFN-γ+ IL17+
**
***
***
PBS
P3
MOG35-55

Figure 7


A
TCR beta
TCR alpha
Peptide 3
MHCII
B
Peptide-TCR
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TCR beta CDR3
Arg
Pro
Peptide 3
P3: TTLSFYRPPFLRVRRPFYIIF
Peptide-MHC II
MHCII
Phe
Pro
Leu
Arg
Thr
Ser
Arg
Phe
Leu
Pro
Tyr
Peptide 3
C
PBS
MOG35-55
P3
Relative cells number
5.89
94.0
29.9
CFSE
D
****
****
% Proliferation
100
80
60
40
20
0
PBS
MOG35-55
P3
**
**
% of CD69+ cells in CD4+ T cells
80
60
40
20
0
PBS
MOG35-55
P3